Docket JP920030152US1

Appl. No.: 10/699,024
Filing Date: October 31, 2003

IN THE CLAIMS

Please amend the claims as follows:

1. (currently amended) A method for presenting sequence data by a computer system, the method comprising the steps of:

identifying initial replets and at least one additional replet by the computer system, for sequence data in a memory accessible by the computer system, wherein the initial and additional replets represent respective parts of said sequence data;

storing in a memory accessible by the computer system for each initial and additional replet, at least ~~one~~ two position-match parameters ~~entry that records~~ for recording a respective at least one data position of the replet within the sequence data;

generating a certain ~~backbone~~ data sequence, wherein generating the certain ~~backbone~~ data sequence includes the computer system removing the initial replets from the sequence data; and

presenting ~~the sequence data as~~ the certain ~~backbone~~ data sequence to a user in combination with the position-match entries, wherein the position match parameters for each initial and additional replet enable selecting between reconstructing the sequence data responsive to i) the initial replets without the at least one additional replet and ii) the initial replets with the at least one additional replet.

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2. (currently amended) The method as claimed in claim 1, further comprising the steps of:

associating ~~ones of~~ the initial and at least one additional replets with respective subsequences of the data sequence; and

storing portions of the subsequences as data variation portions, wherein the data variation portions of the subsequences differ from their respectively identified replets.

3. (currently amended) The method as claimed in claim 2, wherein the step of storing data variations is performed using a pointer ~~indirection~~.

4. (currently amended) The method as claimed in claim 1, further comprising the step of:

identifying, among said identified initial and additional replets, certain ~~meta-~~replets that can be used to represent multiple replets.

5. (currently amended) The method as claimed in claim 4, further comprising the step of:

segmenting the certain ~~meta-~~replets into multiple parts to account for location-specific variations of the certain ~~meta-~~replets in the sequence data.

6. (currently amended) The method as claimed in claim 1, further comprising the step of:

storing replet information in a replet-information table using a pointer, ~~indirection~~ so that equivalent sequences occupy single storage space.

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7. (currently amended) The method as claimed in claim 1, further comprising the step of:

identifying subsequences of the sequence data able to be represented by one or more different <u>ones of the initial and at least one additional</u> replets.

8. (currently amended) The method as claimed in claim 7, further comprising the step of:

storing only one of said <u>initial or at least one additional</u> replets able represent the identified subsequences.

9. (currently amended) The method as claimed in claim 1, further comprising the step of:

identifying patterns common to the identified <u>initial</u> replets <u>or common to the initial and at least one additional replets</u>.

10. (previously presented) The method as claimed in claim 1, further comprising the step of:

storing multiple views of the sequence data at multiple levels of abstraction.

11. (currently amended) The method as claimed in claim 1, further comprising the step of:

storing annotation information for sequence data with corresponding position-match <u>parameters.</u> ~~entries.~~

12-13. (canceled)